SEQUENCE LISTING

<110> JAPAN SCIENCE AND TECHNOLOGY CORPORATION

<120> Regucalcin gene-transferred non-human animals

<130> YG2002-18PCT

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<150> JP P2001-287698
<151> 2001-9-20

<150> JP P2002-177666
<151> 2002-6-18

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<170> PatentIn Ver. 2.1

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Gly Glu Ser Pro Val Trp Glu Glu Ala Ser Lys Cys Leu Leu Phe Val
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gac atc cct tca aag act gtc tgc cga tgg gat tcg atc agc aat cga   144
Asp Ile Pro Ser Lys Thr Val Cys Arg Trp Asp Ser Ile Ser Asn Arg
        35                  40                  45

gtg cag cga gtt ggt gta gat gcc cca gtc agt tca gtg gca ctt cga   192
Val Gln Arg Val Gly Val Asp Ala Pro Val Ser Ser Val Ala Leu Arg
    50                  55                  60

cag tca gga ggc tat gtt gcc acc att gga acc aag ttc tgt gct ttg   240
Gln Ser Gly Gly Tyr Val Ala Thr Ile Gly Thr Lys Phe Cys Ala Leu
65                  70                  75                  80

aac tgg gaa gat caa tca gta ttt atc cta gcc atg gtg gat gaa gat   288
Asn Trp Glu Asp Gln Ser Val Phe Ile Leu Ala Met Val Asp Glu Asp
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aag aaa aac aat cga ttc aat gat ggg aag gtg gat cct gct ggg aga   336
Lys Lys Asn Asn Arg Phe Asn Asp Gly Lys Val Asp Pro Ala Gly Arg
            100                 105                 110

tac ttt gct ggt acc atg gct gag gaa acc gcc cca gct gtt ctg gag   384
Tyr Phe Ala Gly Thr Met Ala Glu Glu Thr Ala Pro Ala Val Leu Glu
        115                 120                 125

cgg cac caa ggg tcc ttg tac tcc ctt ttt cct gat cac agt gtg aag   432
Arg His Gln Gly Ser Leu Tyr Ser Leu Phe Pro Asp His Ser Val Lys
    130                 135                 140

aaa tac ttt aac caa gtg gat atc tcc aat ggt ttg gat tgg tcc ctg   480
Lys Tyr Phe Asn Gln Val Asp Ile Ser Asn Gly Leu Asp Trp Ser Leu
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gac cat aaa atc ttc tac tac att gac agc ctg tcc tac act gtg gat   528
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Asp His Lys Ile Phe Tyr Tyr Ile Asp Ser Leu Ser Tyr Thr Val Asp
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gcc ttt gac tat gac ctg cca aca gga cag att tcc aac cgc agg act   576
Ala Phe Asp Tyr Asp Leu Pro Thr Gly Gln Ile Ser Asn Arg Arg Thr
            180                 185                 190

gtt tac aag atg gaa aaa gat gaa caa atc cca gat gga atg tgc att   624
Val Tyr Lys Met Glu Lys Asp Glu Gln Ile Pro Asp Gly Met Cys Ile
        195                 200                 205

gat gtt gag ggg aag ctt tgg gtg gcc tgt tac aat gga gga aga gta   672
Asp Val Glu Gly Lys Leu Trp Val Ala Cys Tyr Asn Gly Gly Arg Val
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att cgc cta gat cct gag aca ggg aaa aga ctg caa act gtg aag ttg   720
Ile Arg Leu Asp Pro Glu Thr Gly Lys Arg Leu Gln Thr Val Lys Leu
225                 230                 235                 240

cct gtt gat aaa aca act tca tgc tgc ttt gga ggg aag gat tac tct   768
Pro Val Asp Lys Thr Thr Ser Cys Cys Phe Gly Gly Lys Asp Tyr Ser
                245                 250                 255

gaa atg tac gtg aca tgt gcc agg gat ggg atg agc gcc gaa ggt ctt   816
Glu Met Tyr Val Thr Cys Ala Arg Asp Gly Met Ser Ala Glu Gly Leu
            260                 265                 270

ttg agg cag cct gat gct ggt aac att ttc aag ata aca ggt ctt ggg   864
Leu Arg Gln Pro Asp Ala Gly Asn Ile Phe Lys Ile Thr Gly Leu Gly
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Asp Ile Pro Ser Lys Thr Val Cys Arg Trp Asp Ser Ile Ser Asn Arg
        35                  40                  45
Val Gln Arg Val Gly Val Asp Ala Pro Val Ser Ser Val Ala Leu Arg
    50                  55                  60
Gln Ser Gly Gly Tyr Val Ala Thr Ile Gly Thr Lys Phe Cys Ala Leu
65                  70                  75                  80
Asn Trp Glu Asp Gln Ser Val Phe Ile Leu Ala Met Val Asp Glu Asp
                85                  90                  95
Lys Lys Asn Asn Arg Phe Asn Asp Gly Lys Val Asp Pro Ala Gly Arg
            100                 105                 110
Tyr Phe Ala Gly Thr Met Ala Glu Glu Thr Ala Pro Ala Val Leu Glu
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Arg His Gln Gly Ser Leu Tyr Ser Leu Phe Pro Asp His Ser Val Lys
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Lys Tyr Phe Asn Gln Val Asp Ile Ser Asn Gly Leu Asp Trp Ser Leu
145                 150                 155                 160
Asp His Lys Ile Phe Tyr Tyr Ile Asp Ser Leu Ser Tyr Thr Val Asp
                165                 170                 175
Ala Phe Asp Tyr Asp Leu Pro Thr Gly Gln Ile Ser Asn Arg Arg Thr
            180                 185                 190
Val Tyr Lys Met Glu Lys Asp Glu Gln Ile Pro Asp Gly Met Cys Ile
        195                 200                 205
Asp Val Glu Gly Lys Leu Trp Val Ala Cys Tyr Asn Gly Gly Arg Val
    210                 215                 220
Ile Arg Leu Asp Pro Glu Thr Gly Lys Arg Leu Gln Thr Val Lys Leu
225                 230                 235                 240
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Pro Val Asp Lys Thr Thr Ser Cys Cys Phe Gly Gly Lys Asp Tyr Ser
                245                 250                 255
Glu Met Tyr Val Thr Cys Ala Arg Asp Gly Met Ser Ala Glu Gly Leu
            260                 265                 270
Leu Arg Gln Pro Asp Ala Gly Asn Ile Phe Lys Ile Thr Gly Leu Gly
        275                 280                 285
Val Lys Gly Ile Ala Pro Tyr Ser Tyr Ala Gly
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